

SEQUENCE LISTING

<110> SEKISUI CHEMICAL CO., LTD.  
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<120> EXPRESSION VECTOR, HOST, FUSED PROTEIN, PROCESS FOR PRODUCING  
FUSED PROTEIN AND PROCESS FOR PRODUCING PROTEIN

<130> Q83564

<150> PCT/JP2003/008020  
<151> 2003-06-25

<150> JP 2002-185020  
<151> 2002-06-25

<160> 30

<170> PatentIn version 3.3

<210> 1  
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<213> Pyrococcus horikoshii

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35 40 45

Ile Ile Val Gly Ala Gly His Val Ile Ser Gly Leu Asp Lys Arg Leu  
50 55 60

Val Gly Leu Glu Val Gly Lys Lys Tyr Thr Leu Glu Val Pro Pro Glu  
65 70 75 80

Glu Gly Phe Gly Leu Arg Asp Pro Lys Leu Ile Lys Val Phe Thr Met  
85 90 95

Gly Gln Phe Arg Lys Gln Gly Ile Val Pro Phe Pro Gly Leu Glu Val  
100 105 110

Glu Val Thr Thr Asp Asn Gly Arg Lys Met Lys Gly Arg Val Ile Thr  
115 120 125

Val Ser Gly Gly Arg Val Arg Val Asp Phe Asn His Pro Leu Ala Gly  
130 135 140

Lys Thr Leu Ile Tyr Glu Val Glu Ile Val Glu Lys Ile Glu Asp Pro  
145 150 155 160

Ile Glu Lys Ile Lys Ala Leu Ile Glu Leu Arg Leu Pro Met Ile Asp  
165 170 175

Arg Asp Lys Val Ile Ile Glu Val Gly Glu Lys Asp Val Lys Val Asn  
180 185 190

Phe Gly Glu Gln Asp Val Asp Pro Lys Thr Leu Ile Leu Gly Glu Ile  
195 200 205

Leu Leu Glu Ser Asp Ile Lys Phe Leu Gly Tyr Glu Lys Val Glu Phe  
210 215 220

Lys Pro Ser Val Glu Glu Leu Leu Arg Pro Lys Gln Glu Glu Pro Val  
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Glu Glu Glu Lys Lys Glu Glu Gln Glu Glu Ser Glu Glu Ala Gln Ser  
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Ser

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Lys Glu Asn Lys Ile Tyr Tyr Pro Glu Arg Glu Tyr Glu Pro Ile Gly  
35 40 45

Phe Ile Val Gly Asn Gly Glu Leu Ile Glu Gly Phe Glu Glu Ala Val  
50 55 60

Ile Gly Met Glu Val Gly Glu Glu Lys Thr Val Thr Ile Pro Pro Glu  
65 70 75 80

Lys Gly Tyr Gly Leu Arg Asp Glu Arg Leu Ile Gln Glu Ile Pro Lys  
85 90 95

Glu Met Phe Ala Asp Ala Asp Phe Glu Pro Gln Glu Gly Met Leu Ile  
100 105 110

Leu Ala Ser Gly Ile Pro Ala Lys Ile Ile Lys Val Thr Asp Asp Thr  
115 120 125

Val Thr Leu Asp Phe Asn His Glu Leu Ala Gly Lys Glu Leu Lys Phe  
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Thr Ile Lys Val Arg Asp Val Gln Pro Ala Glu Ser Glu  
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Val Asn Val Ala Lys Lys Val Arg Ile Asp Gly Phe Arg Lys Gly Lys  
35 40 45

Val Pro Met Asn Ile Val Ala Gln Arg Tyr Gly Ala Ser Val Arg Gln  
50 55 60

Asp Val Leu Gly Asp Leu Met Ser Arg Asn Phe Ile Asp Ala Ile Ile  
65 70 75 80

Lys Glu Lys Ile Asn Pro Ala Gly Ala Pro Thr Tyr Val Pro Gly Glu  
85 90 95

Tyr Lys Leu Gly Glu Asp Phe Thr Tyr Ser Val Glu Phe Glu Val Tyr  
100 105 110

Pro Glu Val Glu Leu Gln Gly Leu Glu Ala Ile Glu Val Glu Lys Pro  
115 120 125

Ile Val Glu Val Thr Asp Ala Asp Val Asp Gly Met Leu Asp Thr Leu  
130 135 140

Arg Lys Gln Gln Ala Thr Trp Lys Glu Lys Asp Gly Ala Val Glu Ala  
145 150 155 160

Glu Asp Arg Val Thr Ile Asp Phe Thr Gly Ser Val Asp Gly Glu Glu  
165 170 175

Phe Glu Gly Gly Lys Ala Ser Asp Phe Val Leu Ala Met Gly Gln Gly  
180 185 190

Arg Met Ile Pro Gly Phe Glu Asp Gly Ile Lys Gly His Lys Ala Gly  
195 200 205

Glu Glu Phe Thr Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu  
210 215 220

Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Asn Leu Lys Lys Val  
225 230 235 240

Glu Glu Arg Glu Leu Pro Glu Leu Thr Ala Glu Phe Ile Lys Arg Phe  
245 250 255

Gly Val Glu Asp Gly Ser Val Glu Gly Leu Arg Ala Glu Val Arg Lys  
260 265 270

Asn Met Glu Arg Glu Leu Lys Ser Ala Ile Arg Asn Arg Val Lys Ser  
275 280 285

Gln Ala Ile Glu Gly Leu Val Lys Ala Asn Asp Ile Asp Val Pro Ala  
290 295 300

Ala Leu Ile Asp Ser Glu Ile Asp Val Leu Arg Arg Gln Ala Ala Gln  
305 310 315 320

Arg Phe Gly Gly Asn Glu Lys Gln Ala Leu Glu Leu Pro Arg Glu Leu  
325 330 335

Phe Glu Glu Gln Ala Lys Arg Arg Val Val Val Gly Leu Leu Leu Gly  
340 345 350

Glu Val Ile Arg Thr Asn Glu Leu Lys Ala Asp Glu Glu Arg Val Lys  
 355 360 365

Gly Leu Ile Glu Glu Met Ala Ser Ala Tyr Glu Asp Pro Lys Glu Val  
 370 375 380

Ile Glu Phe Tyr Ser Lys Asn Lys Glu Leu Met Asp Asn Met Arg Asn  
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Val Ala Leu Glu Glu Gln Ala Val Glu Ala Val Leu Ala Lys Ala Lys  
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Val Thr Glu Lys Glu Thr Thr Phe Asn Glu Leu Met Asn Gln Gln Ala  
 420 425 430

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Thr Ala Ala Asp Ser Lys Ala Ala Phe Lys Asn Asp Asp Gln Lys Ser  
 35 40 45

Ala Tyr Ala Leu Gly Ala Ser Leu Gly Arg Tyr Met Glu Asn Ser Leu  
 50 55 60

Lys Glu Gln Glu Lys Leu Gly Ile Lys Leu Asp Lys Asp Gln Leu Ile  
 65 70 75 80

Ala Gly Val Gln Asp Ala Phe Ala Asp Lys Ser Lys Leu Ser Asp Gln  
 85 90 95

Glu Ile Glu Gln Thr Leu Gln Ala Phe Glu Ala Arg Val Lys Ser Ser  
 100 105 110

Ala Gln Ala Lys Met Glu Lys Asp Ala Ala Asp Asn Glu Ala Lys Gly  
 115 120 125

Lys Glu Tyr Arg Glu Lys Phe Ala Lys Glu Lys Gly Val Lys Thr Ser  
 130 135 140

Ser Thr Gly Leu Val Tyr Gln Val Val Glu Ala Gly Lys Gly Glu Ala  
 145 150 155 160

Pro Lys Asp Ser Asp Thr Val Val Val Asn Tyr Lys Gly Thr Leu Ile  
 165 170 175

Asp Gly Lys Glu Phe Asp Asn Ser Tyr Thr Arg Gly Glu Pro Leu Ser  
 180 185 190

Phe Arg Leu Asp Gly Val Ile Pro Gly Trp Thr Glu Gly Leu Lys Asn  
 195 200 205

Ile Lys Lys Gly Gly Lys Ile Lys Leu Val Ile Pro Pro Glu Leu Ala  
 210 215 220

Tyr Gly Lys Ala Gly Val Pro Gly Ile Pro Pro Asn Ser Thr Leu Val  
 225 230 235 240

Phe Asp Val Glu Leu Leu Asp Val Lys Pro Ala Pro Lys Ala Asp Ala  
 245 250 255

Lys Pro Glu Ala Asp Ala Lys Ala Ala Asp Ser Ala Lys Lys  
 260 265 270

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 ttcaaaaatg acgatcagaa atcagcttat gcactgggtg cttecgctggg tcgttacatg 180  
 gaaaactctc ttaaagaaca agaaaaactg ggcacaaac tggataaaga tcagctgatc 240  
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 actctgcaag cattcgaagc tcgctgaag tcttctgctc aggcgaagat ggaaaaagac 360  
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 ccgaaagaca gcgatactgt tgtagtgaac tacaaaggta cgctgatcga cggtaaagag 540  
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20 25 30

Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser  
35 40 45

Val Lys Leu Asn Ala Ala Gln Ala Arg Gln Gln Leu Pro Asp Asp Ala  
50 55 60

Thr Leu Arg His Gln Ile Met Glu Arg Leu Ile Met Asp Gln Ile Ile  
65 70 75 80

Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Ser Asp Glu Gln Leu  
85 90 95

Asp Gln Ala Ile Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Leu Asp  
100 105 110

Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Asn Thr Tyr  
115 120 125

Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn  
130 135 140

Glu Val Arg Arg Arg Ile Thr Ile Leu Pro Gln Glu Val Glu Ser Leu  
145 150 155 160

Ala Gln Gln Val Gly Asn Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu  
165 170 175

Ser His Ile Leu Ile Pro Leu Pro Glu Asn Pro Thr Ser Asp Gln Val  
180 185 190

Asn Glu Ala Glu Ser Gln Ala Arg Ala Ile Val Asp Gln Ala Arg Asn  
195 200 205



Gly Ala Asp Phe Gly Lys Leu Ala Ile Ala His Ser Ala Asp Gln Gln  
210 215 220

Ala Leu Asn Gly Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro  
225 230 235 240

Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Gly Asp Ile Val  
245 250 255

Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp  
260 265 270

Leu Arg Gly Glu Ser Lys Asn Ile Ser Val Thr Glu Val His Ala Arg  
275 280 285

His Ile Leu Leu Lys Pro Ser Pro Ile Met Thr Asp Glu Gln Ala Arg  
290 295 300

Val Lys Leu Glu Gln Ile Ala Ala Asp Ile Lys Ser Gly Lys Thr Thr  
305 310 315 320

Phe Ala Ala Ala Ala Lys Glu Phe Ser Gln Asp Pro Gly Ser Ala Asn  
325 330 335

Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala  
340 345 350

Phe Arg Asp Ala Leu Thr Arg Leu Asn Lys Gly Gln Met Ser Ala Pro  
355 360 365

Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg  
370 375 380

Asn Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met  
385 390 395 400

Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Ser Trp Met Gln Glu  
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Gln Arg Ala Ser Ala Tyr Val Lys Ile Leu Ser Asn  
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<210> 8  
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<212> DNA  
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gacgttgatg gattaatgca gtcggtaaaa ctgaacgctg ctcaggcaag gcagcaactt      180
cctgatgacg cgacgctgcg ccaccaaate atggaacggt tgatcatgga tcaaateatc      240
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gatggactga actacaacac ctatcgtaac cagatccgca aagagatgat tatctctgaa      420
gtgcgtaaca acgaggtgcg tcgtcgcate accatcctgc cgcaggaagt cgaatccctg      480
gcgcagcagg tgggtaacca aaacgacgcc agcactgagc tgaacctgag ccacatcctg      540
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<213> Homo sapiens

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<400> 9

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Val Leu Lys Val Ile Lys Arg Glu Gly Thr Gly Thr Glu Met Pro Met  
35 40 45

Ile Gly Asp Arg Val Phe Val His Tyr Thr Gly Trp Leu Leu Asp Gly  
50 55 60

Thr Lys Phe Asp Ser Ser Leu Asp Arg Lys Asp Lys Phe Ser Phe Asp  
65 70 75 80

Leu Gly Lys Gly Glu Val Ile Lys Ala Trp Asp Ile Ala Ile Ala Thr  
85 90 95

Met Lys Val Gly Glu Val Cys His Ile Thr Cys Lys Pro Glu Tyr Ala  
100 105 110

Tyr Gly Ser Ala Gly Ser Pro Pro Lys Ile Pro Pro Asn Ala Thr Leu  
115 120 125

Val Phe Glu Val Glu Leu Phe Glu Phe Lys Gly Glu Asp Leu Thr Glu  
130 135 140

Glu Glu Asp Gly Gly Ile Ile Arg Arg Ile Gln Thr Arg Gly Glu Gly  
145 150 155 160

Tyr Ala Lys Pro Asn Glu Gly Ala Ile Val Glu Val Ala Leu Glu Gly  
165 170 175

Tyr Tyr Lys Asp Lys Leu Phe Asp Gln Arg Glu Leu Arg Phe Glu Ile  
180 185 190

Gly Glu Gly Glu Asn Leu Asp Leu Pro Tyr Gly Leu Glu Arg Ala Ile  
195 200 205

Gln Arg Met Glu Lys Gly Glu His Ser Ile Val Tyr Leu Lys Pro Ser  
210 215 220

Tyr Ala Phe Gly Ser Val Gly Lys Glu Lys Phe Gln Ile Pro Pro Asn  
225 230 235 240

Ala Glu Leu Lys Tyr Glu Leu His Leu Lys Ser Phe Glu Lys Ala Lys  
245 250 255

Glu Ser Trp Glu Met Asn Ser Glu Glu Lys Leu Glu Gln Ser Thr Ile  
260 265 270

Val Lys Glu Arg Gly Thr Val Tyr Phe Lys Glu Gly Lys Tyr Lys Gln  
275 280 285

Ala Leu Leu Gln Tyr Lys Lys Ile Val Ser Trp Leu Glu Tyr Glu Ser  
290 295 300

Ser Phe Ser Asn Glu Glu Ala Gln Lys Ala Gln Ala Leu Arg Leu Ala  
305 310 315 320

Ser His Leu Asn Leu Ala Met Cys His Leu Lys Leu Gln Ala Phe Ser  
325 330 335

Ala Ala Ile Glu Ser Cys Asn Lys Ala Leu Glu Leu Asp Ser Asn Asn  
340 345 350

Glu Lys Gly Leu Phe Arg Arg Gly Glu Ala His Leu Ala Val Asn Asp  
355 360 365

Phe Glu Leu Ala Arg Ala Asp Phe Gln Lys Val Leu Gln Leu Tyr Pro  
370 375 380

Asn Asn Lys Ala Ala Lys Thr Gln Leu Ala Val Cys Gln Gln Arg Ile  
385 390 395 400

Arg Arg Gln Leu Ala Arg Glu Lys Lys Leu Tyr Ala Asn Met Phe Glu  
405 410 415

Arg Leu Ala Glu Glu Glu Asn Lys Ala Lys Ala Glu Ala Ser Ser Gly  
420 425 430

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435 440 445

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450 455

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<212> PRT
<213> Homo sapiens

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<400> 11

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Met Ser His Pro Ser Pro Gln Ala Lys Pro Ser Asn Pro Ser Asn Pro
1           5           10          15

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Arg Val Phe Phe Asp Val Asp Ile Gly Gly Glu Arg Val Gly Arg Ile
          20          25          30

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Val Leu Glu Leu Phe Ala Asp Ile Val Pro Lys Thr Ala Glu Asn Phe
          35          40          45

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Arg Ala Leu Cys Thr Gly Glu Lys Gly Ile Gly His Thr Thr Gly Lys  
50 55 60

Pro Leu His Phe Lys Gly Cys Pro Phe His Arg Ile Ile Lys Lys Phe  
65 70 75 80

Met Ile Gln Gly Gly Asp Phe Ser Asn Gln Asn Gly Thr Gly Gly Glu  
85 90 95

Ser Ile Tyr Gly Glu Lys Phe Glu Asp Glu Asn Phe His Tyr Lys His  
100 105 110

Asp Arg Glu Gly Leu Leu Ser Met Ala Asn Ala Gly Arg Asn Thr Asn  
115 120 125

Gly Ser Gln Phe Phe Ile Thr Thr Val Pro Thr Pro His Leu Asp Gly  
130 135 140

Lys His Val Val Phe Gly Gln Val Ile Lys Gly Ile Gly Val Ala Arg  
145 150 155 160

Ile Leu Glu Asn Val Glu Val Lys Gly Glu Lys Pro Ala Lys Leu Cys  
165 170 175

Val Ile Ala Glu Cys Gly Glu Leu Lys Glu Gly Asp Asp Gly Gly Ile  
180 185 190

Phe Pro Lys Asp Gly Ser Gly Asp Ser His Pro Asp Phe Pro Glu Asp  
195 200 205

Ala Asp Ile Asp Leu Lys Asp Val Asp Lys Ile Leu Leu Ile Thr Glu  
210 215 220

Asp Leu Lys Asn Ile Gly Asn Thr Phe Phe Lys Ser Gln Asn Trp Glu  
225 230 235 240

Met Ala Ile Lys Lys Tyr Ala Glu Val Leu Arg Tyr Val Asp Ser Ser  
245 250 255

Lys Ala Val Ile Glu Thr Ala Asp Arg Ala Lys Leu Gln Pro Ile Ala  
260 265 270

Leu Ser Cys Val Leu Asn Ile Gly Ala Cys Lys Leu Lys Met Ser Asn  
275 280 285

Trp Gln Gly Ala Ile Asp Ser Cys Leu Glu Ala Leu Glu Leu Asp Pro  
 290 295 300

Ser Asn Thr Lys Ala Leu Tyr Arg Arg Ala Gln Gly Trp Gln Gly Leu  
 305 310 315 320

Lys Glu Tyr Asp Gln Ala Leu Ala Asp Leu Lys Lys Ala Gln Gly Ile  
 325 330 335

Ala Pro Glu Asp Lys Ala Ile Gln Ala Glu Leu Leu Lys Val Lys Gln  
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Lys Ile Lys Ala Gln Lys Asp Lys Glu Lys Ala Val Tyr Ala Lys Met  
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Phe Ala  
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 gagacagcag atagagccaa gctgcaacct atagctttta gctgtgtact gaatattggt 840

gcttgtaaac tgaagatgtc aaattggcag ggagcaattg acagttgttt agaggctctt 900  
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aaagaatatg atcaagcatt ggctgatctt aagaaagctc aggggatagc accagaagat 1020  
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Val Ser Tyr Gln Val Ile Thr Ser Leu Leu Leu Gly Thr Leu Ile Phe  
35 40 45

Cys Ala Val Leu Gly Asn Ala Cys Val Val Ala Ala Ile Ala Leu Glu  
50 55 60

Arg Ser Leu Gln Asn Val Ala Asn Tyr Leu Ile Gly Ser Leu Ala Val  
65 70 75 80

Thr Asp Leu Met Val Ser Val Leu Val Leu Pro Met Ala Ala Leu Tyr  
85 90 95

Gln Val Leu Asn Lys Trp Thr Leu Gly Gln Val Thr Cys Asp Leu Phe  
100 105 110

Ile Ala Leu Asp Val Leu Cys Cys Thr Ser Ser Ile Leu His Leu Cys  
115 120 125

Ala Ile Ala Leu Asp Arg Tyr Trp Ala Ile Thr Asp Pro Ile Asp Tyr  
130 135 140

Val Asn Lys Arg Thr Pro Arg Arg Ala Ala Ala Leu Ile Ser Leu Thr  
145 150 155 160

Trp Leu Ile Gly Phe Leu Ile Ser Ile Pro Pro Met Leu Gly Trp Arg  
165 170 175



Thr Pro Glu Asp Arg Ser Asp Pro Asp Ala Cys Thr Ile Ser Lys Asp  
180 185 190

His Gly Tyr Thr Ile Tyr Ser Thr Phe Gly Ala Phe Tyr Ile Pro Leu  
195 200 205

Leu Leu Met Leu Val Leu Tyr Gly Arg Ile Phe Arg Ala Ala Arg Phe  
210 215 220

Arg Ile Arg Lys Thr Val Lys Lys Val Glu Lys Thr Gly Ala Asp Thr  
225 230 235 240

Arg His Gly Ala Ser Pro Ala Pro Gln Pro Lys Lys Ser Val Asn Gly  
245 250 255

Glu Ser Gly Ser Arg Asn Trp Arg Leu Gly Val Glu Ser Lys Ala Gly  
260 265 270

Gly Ala Leu Cys Ala Asn Gly Ala Val Arg Gln Gly Asp Asp Gly Ala  
275 280 285

Ala Leu Glu Val Ile Glu Val His Arg Val Gly Asn Ser Lys Glu His  
290 295 300

Leu Pro Leu Pro Ser Glu Ala Gly Pro Thr Pro Cys Ala Pro Ala Ser  
305 310 315 320

Phe Glu Arg Lys Asn Glu Arg Asn Ala Glu Ala Lys Arg Lys Met Ala  
325 330 335

Leu Ala Arg Glu Arg Lys Thr Val Lys Thr Leu Gly Ile Ile Met Gly  
340 345 350

Thr Phe Ile Leu Cys Trp Leu Pro Phe Phe Ile Val Ala Leu Val Leu  
355 360 365

Pro Phe Cys Glu Ser Ser Cys His Met Pro Thr Leu Leu Gly Ala Ile  
370 375 380

Ile Asn Trp Leu Gly Tyr Ser Asn Ser Leu Leu Asn Pro Val Ile Tyr  
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Cys Lys Phe Cys Arg Gln  
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ctgctgctgg gcacgctcat cttctgcgcg gtgctgggca atgcggtcgt ggtggctgcc 180  
atgccttgg agcgctccct gcagaacgtg gccattatc ttattggctc ttggcggtc 240  
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aagtggacac tgggccaggt aacctgcgac ctgttcatcg cctcgacgt gctgtgctgc 360  
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33